

Characterization of a prognostic four-gene methylation signature associated with radiotherapy for head and neck squamous cell carcinoma

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Abstract. Head and neck squamous cell carcinoma (HNSCC) remains one of the most common malignancies associated with poor prognosis. DNA methylation has emerged as an important mechanism underlying the radio-resistance of tumors. Prognostic biomarkers based on radiotherapy-related aberrant DNA methylation are limited. Methylation profiles of 388 patients with HNSCC were acquired from The Cancer Genome Atlas (TCGA) portal. Genes with differentially methylated CpG sites (DMGs) were screened between patients with a favorable and poor prognosis with or without radiotherapy. A weight gene co-methylation network was constructed using a Weighted Gene Co-expression Network Analysis (WGCNA) package. A lasso Cox-PH model was used to identify the optimal panel of genes with the ability to predict survival in these patients. Prognostic performance of the multi-gene methylation signature was assessed in a training set and confirmed in a validation set. A total of 976 DMGs were observed between favorable and poor prognostic samples. Four DMG-enriched co-methylation modules were identified. A four-gene methylation signature was determined by the lasso Cox-PH model that consisted of *ZNF10*, *TMPRSS12*, *ERGIC2*, and *RNF215*. The risk score based on the four-gene signature was able to divide the training or validation set into two risk groups with significantly different overall survival. Thus, the present study revealed a radiotherapy-related four-gene methylation signature to predict survival outcomes of patients with

HNSCC, providing candidate therapeutic targets for novel therapy against HNSCC. However, substantial validation experiments are required.

Introduction

Head and neck squamous cell carcinoma (HNSCC) refers to a group of malignancies that originates in the oral cavity, oropharynx, larynx, or hypopharynx (1,2). It is the seventh most common cancer worldwide with an annual incidence of more than half a million (3). The average 5-year overall survival (OS) of patients with HNSCC is between 42-64% (4). Given the intrinsic heterogeneity of this disease, the identification of prognostic gene signatures is of a particular interest to improve HNSCC diagnosis.

DNA methylation patterns are largely altered in cancer cells as compared with normal cells (5). Epigenetic gene silencing caused by DNA methylation has been widely accepted as an important mechanism of tumorigenesis (6). Studies have revealed the aberrant methylation of multiple genes in HNSCC (7,8). Kostareli *et al* demonstrated and confirmed a human papilloma virus (HPV)-related prognostic methylation score for patients with HNSCC (9,10). Moreover, a recent study identified an HPV infection-related epigenetic signature consisting of five CpGs as survival predictors in HPV-positive HNSCC (11). Despite these marked findings, there is a lack of a reliable methylation prognostic signature for risk stratification in patients with HNSCC.

Similar to surgery, radiotherapy alone may be used for HNSCC treatment at early stages. For patients with HNSCC in middle and late stages, radiotherapy is generally implemented in combination with surgical excision that may decrease local recurrence and improve tumor control and the survival of patients (12). DNA methylation is known to play a critical role in the resistance of tumors to radiotherapy (13). Epigenetic silencing of tumor suppressor genes by methylation was revealed to be associated with radio-resistance of oral squamous cell carcinoma and poor outcome of patients (14). Given the close associations between DNA methylation and radiotherapy, herein we focused on the identification of a prognostic methylation signature from radiotherapy-related differentially methylated CpG sites based on the methylation data obtained from 388 patients with HNSCC from The Cancer Genome Atlas (TCGA) database. The prognostic robustness of this

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Abbreviations: HNSCC, head and neck squamous cell carcinoma; TCGA, The Cancer Genome Atlas; DMG, differentially methylated CpG site; WGCNA, Weighted Gene Co-expression Network Analysis; HPV, human papilloma virus; OS, overall survival; FDR, false discovery rate; FC, fold change

Key words: HNSCC, DNA methylation, prognostic signature, radiotherapy, WGCNA

methylation signature was assessed in a training set as well as a validation set.

Materials and methods

Retrieval of public data. The DNA methylation profile of 580 patients with HNSCC was retrieved from TCGA data portal (<https://tcga-data.nci.nih.gov/tcga/>) based on the Illumina Infinium Human Methylation 450 BeadChip platform. Of these patients, 388 with corresponding clinical data concerning radiotherapy and survival were selected as a training cohort. The GSE75537 (15) dataset downloaded from the National Center for Biotechnology Information Gene Expression Omnibus repositories (<http://www.ncbi.nlm.nih.gov/geo/>) contained 108 samples of oral tongue squamous cell carcinomas, and 53 of these samples with available survival information were selected as a validation cohort.

Differential methylation analyses between favorable and poor prognostic samples. Poor prognostic samples (patients not receiving radiotherapy with an OS of 12 months or shorter) and favorable prognostic samples (patients receiving radiotherapy with an OS of 48 months or longer) were selected from the training cohort. The acquired methylated sites were annotated based on the platform annotation information, and only those in the CpGs sites were retained. The genes with differentially methylated CpG sites (DMGs) between the two groups were selected using the limma package (16) (version 3.34.7, <https://bioconductor.org/packages/release/bioc/html/limma.html>) with significant cut-off values of false discovery rate (FDR) <0.05 and \log_2 fold change (FC) >0.1.

Selection of co-methylation modules. A weighted gene co-methylation network with all methylated CpGs obtained from the training set was constructed using the Weighted Gene Co-expression Network Analysis (WGCNA) software (17,18) (<https://cran.r-project.org/web/packages/WGCNA/index.html>). To achieve scale-free topology, a soft-thresholding power of $\beta=5$ with a scale-free R^2 value of 0.9 for calculating adjacency, was selected. The genes with similar methylation levels were grouped into the same module. The modules with $\text{minSize}=100$ and $\text{cutHeight}=0.95$ were identified by dynamic tree cut algorithm using *dynamicTreeCut* version 1.63 (<https://cran.r-project.org/web/packages/dynamicTreeCut/index.html>). Enrichment analysis of DMGs was carried out in each identified module with a hypergeometric-based test (19). The modules with $P<0.05$ and fold enrichment >1 were selected as DMG-enriched modules, which were subjected to gene ontology (GO) (20) functional enrichment analysis using the DAVID (<https://david.ncifcrf.gov/>) bioinformatics online tool (21).

Correlation analysis of methylation and expression data. Methylation and expression data of the DMGs were focused on in these selected DMG-enriched modules. Using methylation data and the matched mRNA expression data, overall methylation levels of all DMGs and their overall gene expression levels were correlated by calculating Pearson correlation coefficient (CC) using the *cor.test* function (<https://stat.ethz.ch/R-manual/R-devel/library/stats/html/cor.test.html>). Correlation between

Table I. Clinical covariates of patients in the training set and the validation set.

Clinical covariates	Training set (n=388)	Validation set (n=53)
Age (mean \pm SD, years)	60.81 \pm 11.66	49.36 \pm 13.47
Sex (male/female)	288/100	42/11
Death (dead/alive/-)	117/271	15/38
OS time (mean \pm SD, months)	26.43 \pm 26.21	30.46 \pm 26.98

OS, overall survival; SD, standard deviation.

methylation levels and expression levels was explored for every individual DMG. As a result, the genes with a negative CC value were selected for further analysis.

Statistical analysis for survival. Based on the survival information of patients in the training set, a univariate Cox regression analysis was performed to evaluate the association of the aforementioned genes which had a negative CC with prognosis. The significant genes with a log-rank $P<0.05$ were regarded as prognosis-related genes, which were used as input for a L1 penalized (LASSO) Cox-proportional hazard (PH) model (22) to identify the optimal panel of prognostic genes using the penalized package (<https://cran.r-project.org/web/packages/penalized/>) of R language (version 3.4.1). Cox-PH coefficients and methylation levels of these prognostic genes were combined to construct the following prognostic model:

$$\text{Risk score} = \sum \text{coef}_{\text{gene}} \times \text{Methylation}_{\text{gene}}$$

where, $\text{Coef}_{\text{gene}}$ represents the Cox-PH coefficient of an individual gene; and $\text{Methylation}_{\text{gene}}$ represents the methylation level of an individual gene.

A risk score was assigned to each sample in the training cohort. With a median methylation risk score as the cutoff, the training set was dichotomized into a high-risk group and a low-risk group. Survival probabilities of the two groups were analyzed by Kaplan-Meier estimates (23) using survival package of R language. P-values from the log-rank test suggested significance of the prognostic model. Specificity and sensitivity of this model were assessed by the area under the receiver operating characteristic (ROC) curve (AUC) analysis. Prognostic performance of the methylation signature was assessed in the validation cohort.

Results

Identification of radiotherapy-related DMGs. Clinical and demographic data of the training and validation cohorts are presented in Table I. Based on the aforementioned criterion of sample classification, the training cohort had 30 poor prognostic samples and 27 favorable prognostic samples. Between the poor and favorable prognostic samples, a total of 976 DMGs associated with radiotherapy ($3.43 \times 10^{-8} < P_{\text{nominal}} < 6.807 \times 10^{-4}$, FDR <0.05) were obtained by differential methylation analysis (Fig. 1A). Among these DMGs, 476 (48.77%)

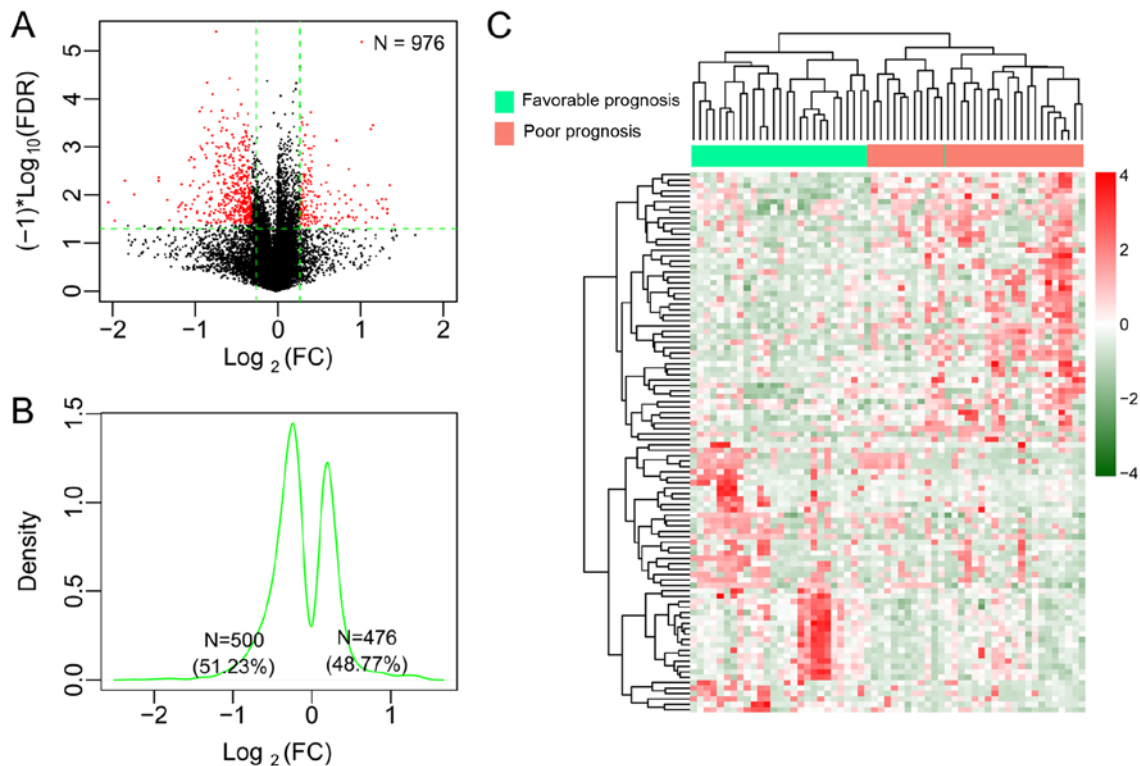


Figure 1. Analysis of DMGs between favorable and poor prognostic samples of the training set. (A) Volcano plot of effect size (\log_2 [fold changes]) against $-\log_{10}(\text{FDR})$ of DMGs. The red spots stand for DMGs with $\text{FDR} < 0.05$ and $|\log_2\text{FC}| > 0.1$, while black spots stand for non-significant DMGs. The horizontal green dash line denotes $\text{FDR} < 0.05$; the vertical green dash lines denote $|\log_2\text{FC}| > 0.1$. (B) Kernel density plot of \log_2 (fold changes) of DMGs. (C) Two-way hierarchical clustering analysis of favorable and poor prognostic samples based on methylation levels of the top 100 DMGs. Color mapping from green to red indicates methylation level from low to high. DMGs, differentially methylated CpG sites; FDR, false discovery rate.

were hypermethylated and 500, hypomethylated (Fig. 1B). The two-way hierarchical clustering analysis based on methylation levels of the top 100 DMGs revealed the difference in the DNA methylation pattern between the favorable prognostic samples and the poor prognostic samples (Fig. 1C). With regard to the CpG sites in the 976 DMGs, 192 DMGs were located in the TSS region, 220 in the gene body region, 30 in the first exon, 53 in the 5'-untranslated regions (UTRs), 35 in the 3'-UTRs, and 446 in the promoters. All significant DMGs were ranked according to the FDR value. As a consequence, the top 20 DMGs with significance were selected (Table II).

WGCNA network analysis and key module identification.

To evaluate the correlation between all methylated CpGs obtained from the training dataset, a weighted gene co-methylation network was applied to these methylated CpGs. Twelve modules of co-methylated genes were identified, wherein CC varied from 0.514 to 0.772 (mean value=0.642, Table III and Fig. 2A). Other CpGs that exhibited no significant correlation with methylation levels were grouped into a grey module. The enrichment of DMGs was evaluated in these modules. As revealed in Fig. 2B and C, yellow-green, magenta, purple, and turquoise modules had 44, 92, 45 and 113 DMGs, respectively, and each of these met the criteria of fold enrichment > 1 and $P < 0.05$. Thus, the four DMG-enriched modules were subjected to GO enrichment analysis. All DMGs in the four modules were predominately linked to protein-DNA complex assembly, nucleosome organization, chromatin assembly, and the cell cycle process (Table IV).

Identification and validation of a four-gene prognostic methylation signature.

In correlation analysis, an inverse correlation was evident between overall methylation and overall expression of all DMGs in the four DMG-enriched modules ($\text{CC} = -0.5051$, $P = 2.20 \times 10^{-16}$; Fig. 3). In addition, an inverse correlation was also observed between methylation and gene expression of individual genes for 165 genes. Univariate Cox regression analysis revealed that 34 genes were significantly related to prognosis in methylation levels, 41 genes had a significant association with prognosis in gene expression levels, and 10 were overlapped (Fig. 4).

A lasso Cox-PH model was fit using the overlapped 10 genes to identify the optimal panel of methylation genes for prognosis prediction. The parameter λ value was tuned to 0.1845 by conducting 1,000 simulations of cross-validation to obtain a maximal cross-validation likelihood (cvl) value of -720.354. A panel of four genes was obtained under this condition, including zinc finger protein (*ZNF*)10, transmembrane serine protease (*TMPRSS*)12, endoplasmic reticulum-Golgi intermediate compartment protein (*ERGIC*)2, and ring finger protein (*RNF*)215.

It was investigated whether the methylation level of the four genes was associated with prognosis. As revealed in Fig. 5A, all patients from the training set were divided into hypermethylated and hypomethylated groups based on the median methylation level of each gene. A Kaplan-Meier plot revealed that the patients with hypomethylated *ZNF10* had significantly better survival outcome than those with hypermethylated *ZNF10* ($P = 0.0434$). The same result

Table II. Top 20 DMGs between favorable and poor prognostic samples.

ID	Chr	Position	Gene	Location	β -favorable	β -poor	Effect	Pnominal	FDR
cg26934993	chr17	37528248	KAT2A	TSS200	0.3667	0.6062	-0.7253	5.43x10 ⁻⁸	3.980x10 ⁻⁶
cg26370886	chr19	53930240	RASIP1	Body	0.3655	0.5390	-0.5604	5.12x10 ⁻⁷	3.750x10 ⁻⁵
cg24351916	chr3	39427639	RPSA	Body	0.7753	0.8339	-0.1051	5.82x10 ⁻⁷	4.270x10 ⁻⁵
cg09938490	chr15	41876101	SERINC4	Body	0.8672	0.7346	0.2394	8.47x10 ⁻⁷	6.210x10 ⁻⁵
cg08069338	chr6	160127888	SNORA29	TSS1500	0.8294	0.7166	0.2110	9.56x10 ⁻⁷	7.010x10 ⁻⁵
cg27211576	chr15	72880218	CSK	Body	0.6376	0.5534	0.2045	1.60x10 ⁻⁶	1.171x10 ⁻⁴
cg26264697	chr19	3529064	HMG20B	Body	0.4428	0.5928	-0.4210	1.78x10 ⁻⁶	1.307x10 ⁻⁴
cg27266479	chr1	9217469	H6PD	Promoter	0.1574	0.1290	0.2868	1.95x10 ⁻⁶	1.432x10 ⁻⁴
cg21657521	chr19	7650447	C19orf59	TSS1500	0.0907	0.1250	-0.4637	2.75x10 ⁻⁶	2.017x10 ⁻⁴
cg05657416	chr6	27213771	HIST1H4I	TSS1500	0.8716	0.8073	0.1106	2.86x10 ⁻⁶	2.099x10 ⁻⁴
cg21205305	chr19	54884437	C19orf76	Promoter	0.2889	0.3970	-0.4583	3.09x10 ⁻⁶	2.263x10 ⁻⁴
cg27537591	chr10	116687888	TRUB1	Promoter	0.0501	0.0402	0.3154	3.30x10 ⁻⁶	2.422x10 ⁻⁴
cg25739003	chr11	62097836	EEF1G	Promoter	0.0751	0.0606	0.3092	4.23x10 ⁻⁶	3.100x10 ⁻⁴
cg26740494	chr1	1556994	MMP23B	TSS1500	0.4795	0.6275	-0.3881	4.68x10 ⁻⁶	3.434x10 ⁻⁴
cg26222042	chr5	31567957	C5orf22	Promoter	0.0580	0.0447	0.3762	4.68x10 ⁻⁶	3.434x10 ⁻⁴
cg26615259	chr1	154977769	MRPL24	Promoter	0.0558	0.0447	0.3208	4.75x10 ⁻⁶	3.483x10 ⁻⁴
cg27085584	chr5	61735043	DIMT1L	Promoter	0.0392	0.0496	-0.3411	4.85x10 ⁻⁶	3.555x10 ⁻⁴
cg27535410	chr19	797354	PRTN3	Body	0.8207	0.9326	-0.1844	5.20x10 ⁻⁶	3.812x10 ⁻⁴
cg27065374	chrX	67976906	EFNB1	Body	0.5659	0.4863	0.2185	5.20x10 ⁻⁶	3.816x10 ⁻⁴
cg22961457	chr20	61840754	SLC2A4RG	3'UTR	0.2397	0.4364	-0.8641	5.41x10 ⁻⁶	3.965x10 ⁻⁴

β -favorable and β -poor represent the mean methylation level of favorable and poor prognostic samples, respectively. Chr, chromosome; FDR, false discovery rate; DMG, genes with differentially methylated CpG sites.

Table III. WGCNA network analysis identified gene modules with co-methylated CpG sites.

Module color	Count of CpGs	Correlation	Pcorr	Count of DM CpGs	Enrichment fold (95% CI)	Phyper
Black	301	0.702	7.01x10 ⁻³²	30	1.033 (0.679-1.521)	8.43x10 ⁻¹
Blue	562	0.514	1.70x10 ⁻⁶	38	0.701 (0.486-0.985)	4.01x10 ⁻²
Brown	469	0.689	6.68x10 ⁻¹¹	28	0.619 (0.403-0.915)	1.31x10 ⁻²
Green	397	0.561	1.33x10 ⁻⁷	46	1.201 (0.856-1.652)	2.63x10 ⁻¹
Green-yellow	196	0.687	2.14x10 ⁻³³	44	2.327 (1.622-3.277)	5.59x10 ⁻⁶
Grey	2,623	0.215	8.56x10 ⁻²	180	0.711 (0.596-0.846)	7.10x10 ⁻⁵
Magenta	221	0.642	7.05x10 ⁻¹⁰	92	4.314 (3.301-5.604)	2.20x10 ⁻¹⁶
Pink	248	0.565	1.59x10 ⁻⁴	2	0.084 (0.010-0.306)	9.75x10 ⁻⁸
Purple	208	0.687	2.71x10 ⁻²³	45	2.243 (1.571-3.142)	1.00x10 ⁻⁵
Red	324	0.701	5.87x10 ⁻⁴	13	0.416 (0.218-0.727)	6.86x10 ⁻⁴
Tan	182	0.772	4.53x10 ⁻²⁶	16	0.911 (0.507-1.532)	8.99x10 ⁻¹
Turquoise	649	0.645	1.47x10 ⁻²⁷	113	1.805 (1.442-2.245)	2.96x10 ⁻⁷
Yellow	431	0.538	1.66x10 ⁻¹⁵	10	0.241 (0.114-0.449)	4.86x10 ⁻⁸

WGCNA, Weighted Gene Co-expression Network Analysis; Count of CpGs, the number of CpGs in a module; Count of DM CpGs, the number of differentially methylated CpGs enriched in a module; Pcorr, P-value for correlation coefficient; Phyper, P-value for enrichment analysis.

was observed for *TMPRSS12* (P=0.0386) and *ERGIC2* (P=3.093x10⁻⁴). Conversely, a significantly worse prognosis was observed in the patients with hypomethylated *RNF215* as compared to those with hypermethylated *RNF215* (P=0.0129).

The relationship between gene expression of each of the four genes and survival was explored. Based on the median gene expression level, all samples in the training set were classified into high expression and low expression groups. *ZNF10*, *TMPRSS12* and *ERGIC2* were associated with significantly

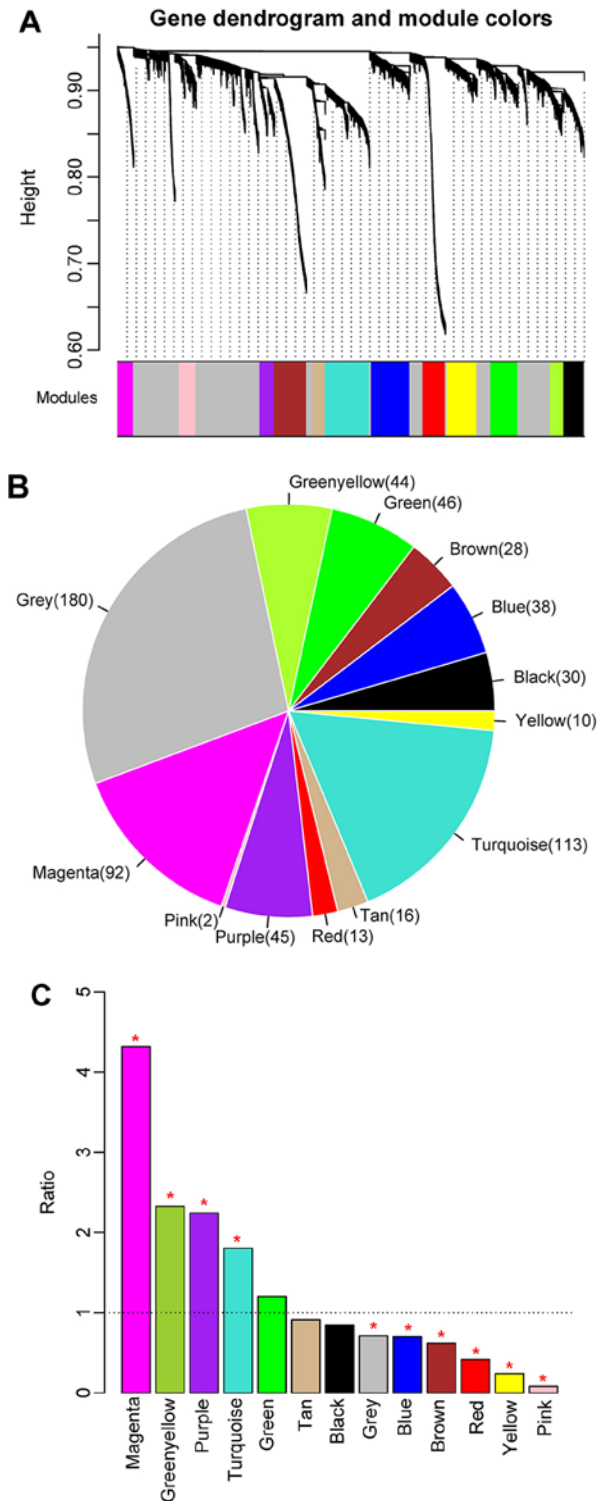


Figure 2. Results of the WGCNA. (A) Clustering dendrograms of gene modules associated with co-methylated CpG sites. Genes in the same branch were highly connected. Each color indicates a certain gene. (B) The count of significant DMGs mapped in each gene module. Each color represents a gene module, and the number represents the genes with differentially methylated CpGs. (C) Fold-enrichment value of each module. The vertical axis stands for the fold enrichment value. The horizontal black dash line denotes fold enrichment=1. *P<0.05. WGCNA, Weighted Gene Co-expression Network Analysis; DMGs, differentially methylated CpG sites.

longer OS in the high expression group than in the low expression group (P=1.125x10⁻⁴, P=0.0471, P=1.196x10⁻³; Fig. 5B). An opposite result was observed for *RNF215*; patients with

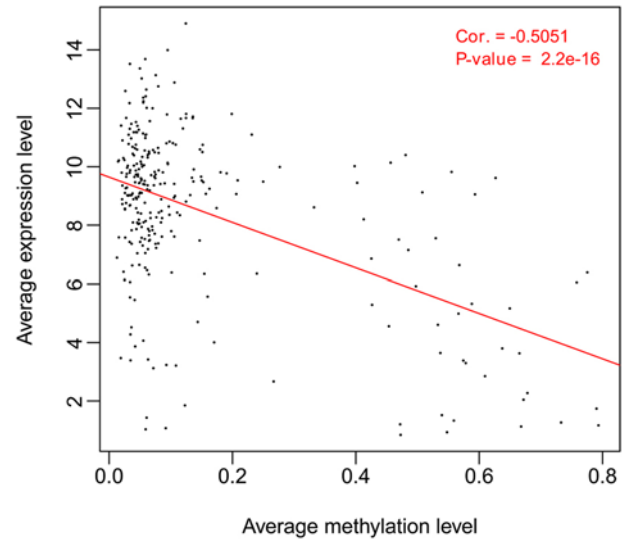


Figure 3. Scatter plot of the overall correlation between methylation and gene expression levels of the paired samples in TCGA portal for the 294 genes contained in the significantly enriched four gene modules, yellow-green, magenta, purple, and turquoise modules. The black spots represent genes. The red line is the trend line of the genes. Cor. denotes Pearson's correlation coefficient of methylation and gene expression. The P-value indicates the significance of the correlation.

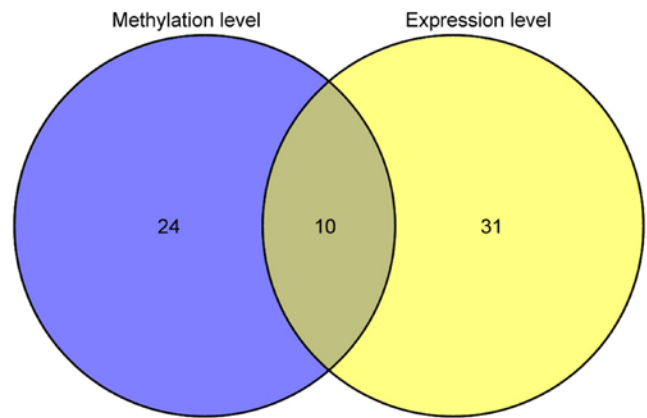


Figure 4. A Venn diagram depicting overlap between the genes significantly related to prognosis in methylation level (left) and the genes significantly associated with prognosis in gene expression (right). Two groups of genes were identified by univariate Cox regression analysis.

high *RNF215* expression had significantly shorter OS than those with low expression (P=0.0391; Fig. 5B).

A risk prediction model was constructed that included risk score based on the Cox-PH prognostic correlation of the optimal four-gene panel (Table V):

$$\text{Risk score} = (0.9639) \times \text{Methylation}_{\text{cg}25577680} + (1.035) \times \text{Methylation}_{\text{cg}27261219} + (7.1664) \times \text{Methylation}_{\text{cg}25338581} + (-4.8961) \times \text{Methylation}_{\text{cg}25964984}$$

The risk score was calculated for each patient. The training cohort was grouped based on the risk score into high-risk and low-risk groups. Samples in the low-risk group exhibited a significantly longer OS than those from the high-risk group (P=7.056x10⁻³; Fig. 6A). The AUC value of the methylation risk score was 0.957, suggestive of the high accuracy of the four-gene methylation signature in predicting the survival of

Table IV. Significantly enriched GO terms for genes with differentially methylated CpGs in four important gene modules.

GO term	Count of genes	P-value	Genes
Protein-DNA complex assembly	8	2.71x10 ⁻⁴	HIST2H2AA3, HIST4H4, HIST1H2AG, HIST1H2BL, CENPA, HIST1H2BG, HIST1H3A, HIST1H2AH, MIS12
Nucleosome organization	8	3.10x10 ⁻⁴	HIST2H2AA3, HIST4H4, HIST1H2AG, HIST1H2BL, CENPA, HIST1H2BG, HIST1H3A, SUPT16H, HIST1H2AH
Protein folding	10	8.25x10 ⁻⁴	GRPEL1, CRYAA, PFDN5, CCT8, C19ORF2, CCT3, CCT6A, DNAJC2, CLPX, PIN1
Nucleosome assembly	7	1.10x10 ⁻³	HIST2H2AA3, HIST4H4, HIST1H2AG, HIST1H2BL, CENPA, HIST1H2BG, HIST1H3A, HIST1H2AH
DNA packaging	8	1.23x10 ⁻³	HIST2H2AA3, CHMP1A, HIST4H4, HIST1H2AG, HIST1H2BL, CENPA, HIST1H2BG, HIST1H3A, HIST1H2AH
Chromatin assembly	7	1.32x10 ⁻³	HIST2H2AA3, HIST4H4, HIST1H2AG, HIST1H2BL, CENPA, HIST1H2BG, HIST1H3A, HIST1H2AH
Chromatin assembly or disassembly	8	1.97x10 ⁻³	HIST2H2AA3, HIST4H4, HIST1H2AG, HIST1H2BL, CENPA, HIST1H2BG, HIST1H3A, SUPT16H, HIST1H2AH
Translation	13	2.31x10 ⁻³	MRPL24, EIF4G1, RPSA, MRPS16, MRPL27, RARS, EIF2S2, RPL35, MARS2, EIF5A, DPH1, RPL10A, MRPL34
Chromosome organization	16	3.19x10 ⁻³	KAT2A, HIST2H2AA3, HIST4H4, HIST1H2AG, HIST1H2BG, NDC80, LIG4, MIS12, C20ORF20, KDM1A, CHMP1A, HIST1H2BL, CENPA, HIST1H3A, SUPT16H, BRE, HIST1H2AH
Cell cycle	21	5.67x10 ⁻³	CCNT2, MAD1L1, CRYAA, NDC80, PMF1, PBK, LIG4, TACC3, ESCO2, UHMK1, MIS12, PIN1, CHMP1A, PSMB6, CENPA, PSMA3, SKA2, RAD51L3, MAPK7, KPNA2, DNAJC2
DNA metabolic process	15	1.11x10 ⁻²	NEIL3, SMC5, PPT1, LIG4, ESCO2, PCNA, SUPT16H, PSIP1, BRE, DDB2, RAD51L3, KPNA2, DNAJC2, APEX1, DUT
Cell cycle process	16	1.24x10 ⁻²	MAD1L1, CRYAA, NDC80, PMF1, PBK, TACC3, UHMK1, MIS12, CHMP1A, PSMB6, CENPA, PSMA3, SKA2, RAD51L3, KPNA2, DNAJC2
Mitotic cell cycle	12	1.44x10 ⁻²	MAD1L1, CHMP1A, PSMB6, CENPA, PSMA3, NDC80, SKA2, PMF1, PBK, DNAJC2, KPNA2, MIS12
Response to DNA damage stimulus	12	1.52x10 ⁻²	NEIL3, DDB2, BRE, SUPT16H, SMC5, PCNA, AATF, RAD51L3, LIG4, ATMIN, APEX1, ESCO2
Chromatin organization	12	1.67x10 ⁻²	KAT2A, KDM1A, HIST2H2AA3, HIST4H4, HIST1H2AG, HIST1H2BL, CENPA, HIST1H2BG, HIST1H3A, BRE, SUPT16H, HIST1H2AH, C20ORF20
M phase	11	1.68x10 ⁻²	MAD1L1, CHMP1A, CRYAA, NDC80, SKA2, RAD51L3, PMF1, PBK, TACC3, KPNA2, MIS12

patients with HNSCC (Fig. 6A). The risk stratification ability of the four-gene methylation signature in the validation cohort was assessed. The validation cohort was classified based on the methylation risk score into high-risk and low-risk groups. The samples in the low-risk group also had markedly longer OS than those from the high-risk group (P=0.0145; Fig. 6B) with an AUC value of 0.905.

Independence of the four-gene prognostic methylation signature from radiotherapy. To investigate whether the prognostic performance of this four-gene methylation signature was independent of radiotherapy, the methylation risk

score was applied to patients with or without radiotherapy. In particular, the patients without radiotherapy were classified based on the methylation risk score into high-risk and low-risk groups, and the OS of patients in the low-risk group was longer than that of patients from the high-risk group (P=3.632x10⁻⁴; Fig. 7A). The patients receiving radiotherapy were also separated as per the methylation risk score into two risk groups, and those from the low-risk group had a significantly longer OS than the patients from the high-risk group (P=0.0281; Fig. 7B). These results demonstrated that the prognostic value of this four-gene methylation signature was independent of radiotherapy.

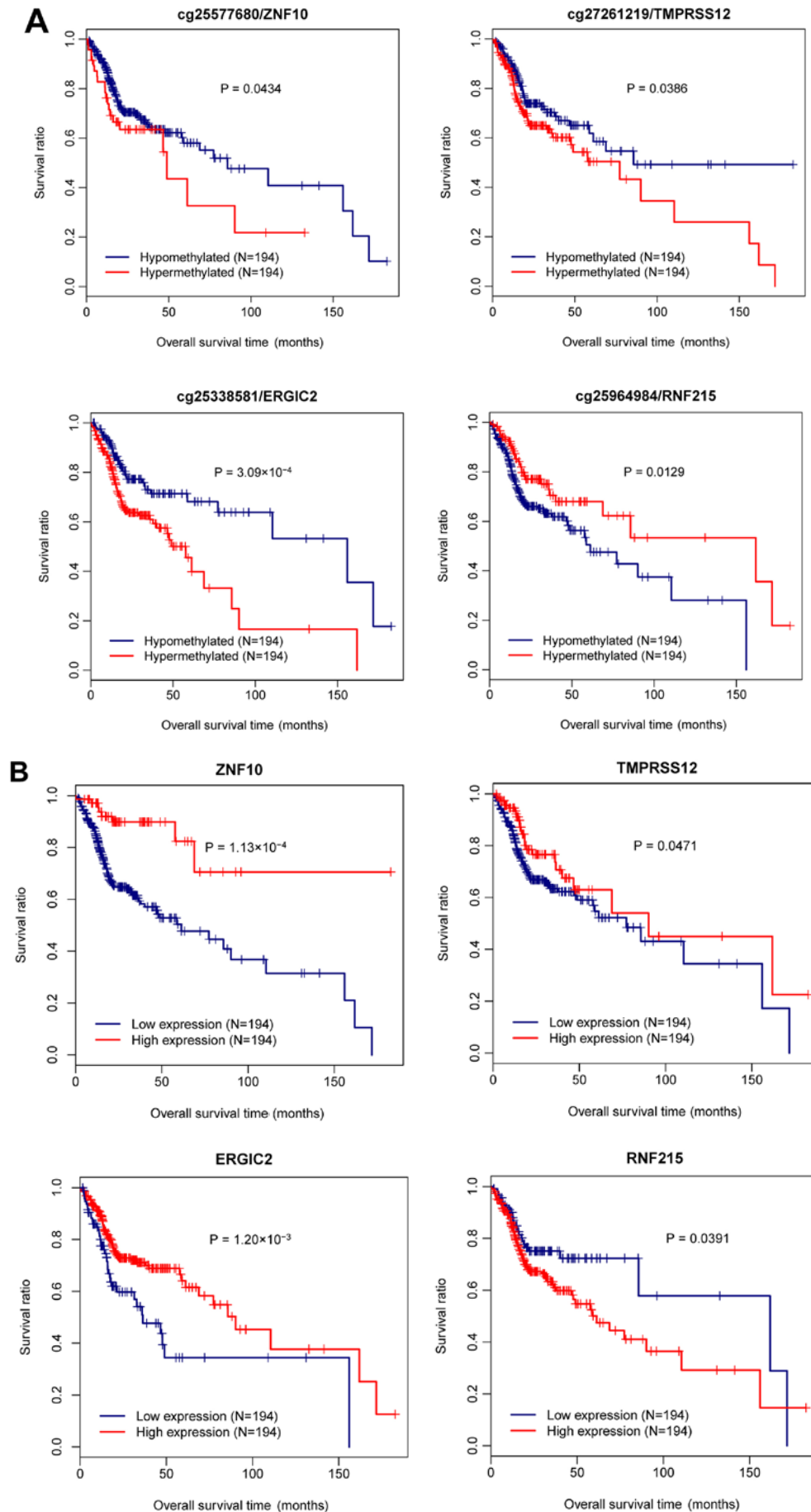


Figure 5. Kaplan-Meier estimates for patients grouped based on (A) median methylation level or (B) median gene expression level of a gene in the training cohort.

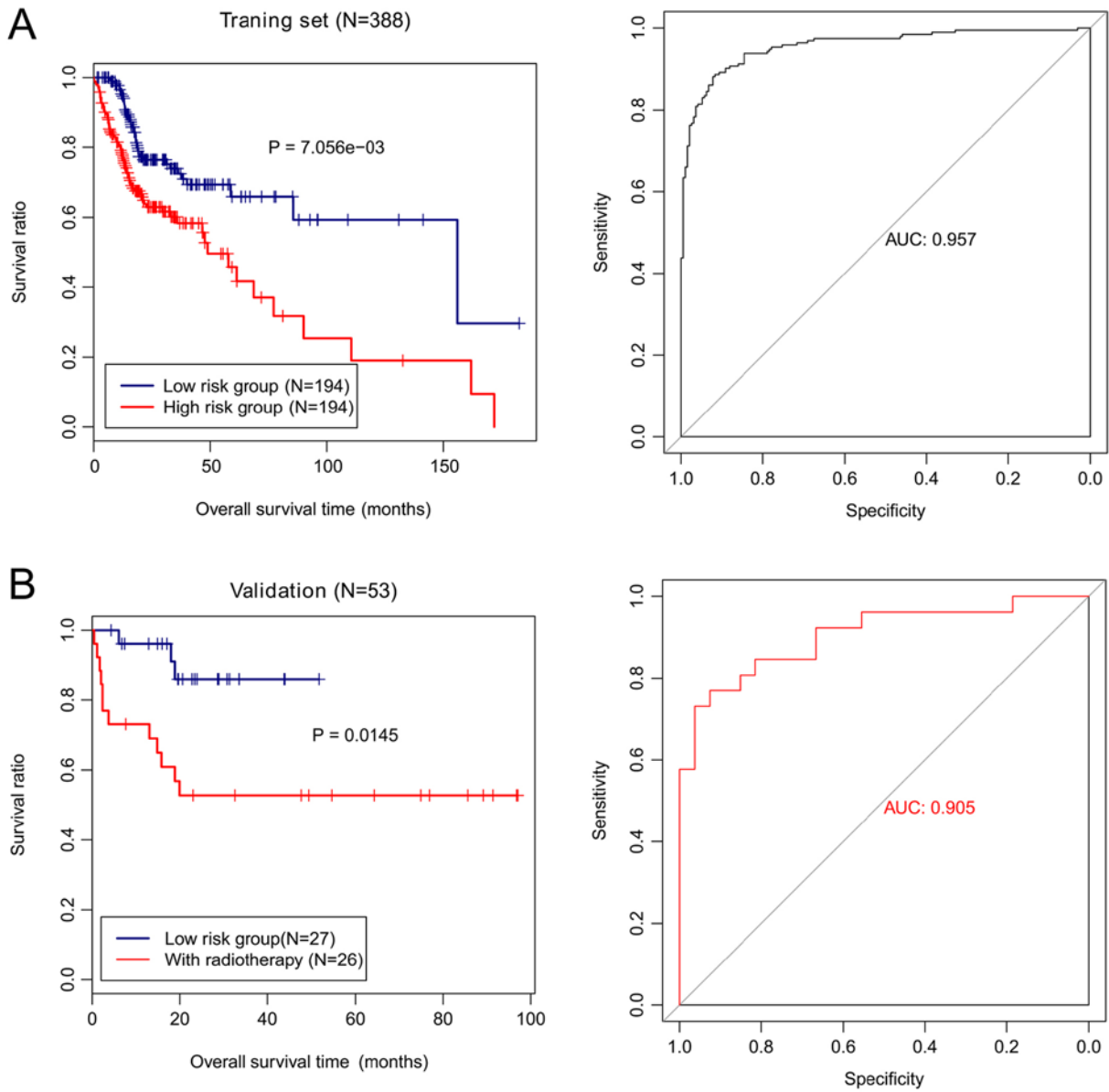


Figure 6. Kaplan-Meier and ROC curves for the four-gene methylation signature in (A) the training set and (B) the validation set. Patients were classified by methylation risk score into high-risk and low-risk groups. Differences between the two groups were evaluated by log-rank test.

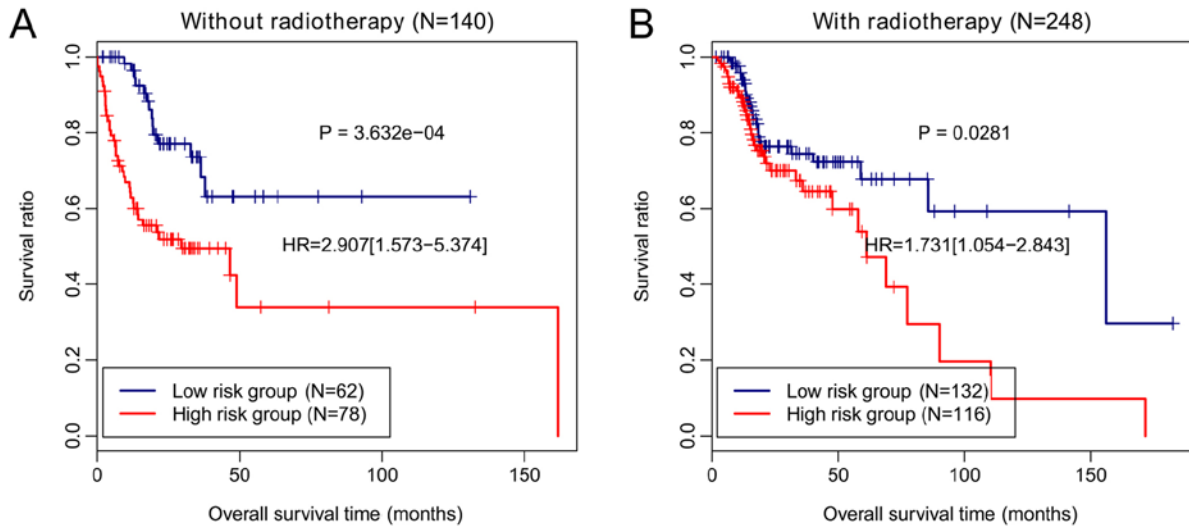


Figure 7. Kaplan-Meier curves for high- and low-risk groups of the patients (A) without or (B) with radiotherapy.

Table V. Risk score model based on a four-gene methylation signature.

ID	Gene	Chr.	Position	Location	Coef	Hazard ratio (95% CI)	P-value
cg25577680	ZNF10	chr12	132217652	Promoter	0.964	6.259 (1.274-10.74)	0.0230
cg27261219	TMPRSS12	chr12	49522905	TSS	1.035	3.179 (1.131-8.935)	0.0277
cg25338581	ERGIC2	chr12	29425828	TSS	7.166	7.576 (4.142-10.506)	0.0023
cg25964984	RNF215	chr22	29113371	TSS	-4.896	0.437 (0.0405-0.719)	0.0223

Chr, chromosome; coef, Cox-PH coefficient.

Discussion

Despite advancements in the diagnosis and treatment of HNSCC, the prognosis remains poor (24). Radiation therapy is used as a standard adjuvant treatment for HNSCC (25). The present study focused on radiotherapy-related aberrant methylation of genes in HNSCC to identify a prognostic methylation signature. A total of 976 DMGs were revealed between the patients with survival of 12 months or shorter without radiotherapy and those surviving for 48 months or longer and receiving radiotherapy. Moreover, four co-methylation modules that were markedly enriched with DMGs were retrieved by WGCNA analysis. The DMGs in the four modules were functionally associated with protein-DNA complex assembly, nucleosome organization, chromatin assembly, and the cell cycle process. These results may improve our understanding of the mechanisms underlying these DNA methylation alterations in HNSCC.

Following correlation analysis and multivariate Cox regression analysis, a LASSO-penalized Cox-PH model was used to identify the most informative genes for the prediction of survival. LASSO is a popular algorithm with a property of simultaneous variable selection and shrinkage, leading to the identification of prognostic signatures (26). It has been used in Cox-PH model for the survival analysis of patients with breast cancer (27). A four-gene panel predictive of prognosis with the lasso Cox-PH model was established. The risk score derived from the four-gene methylation signature stratified the patients into two risk groups with significantly different OS in both the training and validation sets. ROC curves demonstrated high specificity and sensitivity of the four-gene methylation signature in predicting OS of patients with HNSCC.

The four methylation genes of prognostic value were *ZNF10*, *TMPRSS12*, *ERGIC2* and *RNF215*. Zinc finger protein 10 encoded by the *ZNF10* gene acts as a transcription repressor and is a member of the zinc finger proteins, the largest transcription factor family involved in development, differentiation, and metabolism. This protein plays versatile roles in cancer progression (28). Chung *et al* provided evidence that the glioma-associated oncogene family zinc finger 1 is a biomarker in HNSCC (29). However, to the best of our knowledge, the role of *ZNF10* in HNSCC is yet unknown. Based on our results, the hypermethylated CpG sites in *ZNF10* were associated with poor prognosis of patients with HNSCC, suggesting that the hypermethylation of *ZNF10* may serve as an indicator of poor HNSCC prognosis. The *TMPRSS12* gene encodes transmembrane protease, serine 12, a member of the serine protease family participating in diverse

functions such as immune response and blood coagulation and production (30). It has been recognized as an important gene associated with human infertility by genome-wide analyses (31). *TMPRSS12* is used as one of the CG signatures in the identification of cancer-associated aberrant DNA methylation that influences gene expression (32). In our study, it had methylated CpG sites and the hypermethylation was related to poor OS outcome. This observation may suggest that the hypermethylated CpGs in *TMPRSS12* may be the causative factor for poor prognosis of HNSCC. *ERGIC2*, namely *PTX1*, is a gene determined by subtractive hybridization. The *ERGIC2* protein is an endoplasmic reticulum (ER) resident protein implicated in protein trafficking between ER and Golgi bodies (33,34). *PTX1* is an alias for the gene *PITX1*, which has been identified as a predictive indicator of the response to chemotherapy in HNSCC (35). In the present study, as reported for the aforementioned two genes, *ERGIC2* also carried methylated CpG sites, and its hypermethylation was associated with poor survival outcome. Thus, methylated *ERGIC2* may be a predictive factor for HNSCC prognosis. The *RNF125* gene encodes a novel E3 ubiquitin-protein ligase that may be involved in the T-cell receptor signaling pathway (36). Ring finger ubiquitin protein ligases play a role in tumorigenesis and metastasis (37). Yang *et al* suggested that *RNF125* strengthens p53 degradation and suppresses p53 function (38). The proto-oncoprotein S-phase kinase-associated protein2 (Skp2) has been revealed to be overexpressed in many malignancies such as HNSCC. Skp2 plays an important role in the degradation of p27 and p21 via the ubiquitin-proteasome pathway (39). In the present study, the hypomethylation and high expression of *RNF125* were associated with poor OS, indicative of its function as an oncogene in HNSCC. Further studies are warranted to determine if it functions through the ubiquitin-related pathway.

In the present study, it was revealed that the four-gene methylation signature related to radiotherapy can successfully discriminate between the patients with high risk and low risk. The prognostic ability of this methylation signature was independent of radiotherapy. These findings may improve the risk stratification of patients with HNSCC and is of a particular clinical relevance. Despite these valuable findings, the present study has a few limitations. First, the number of patient samples with available clinical information was small. In addition, these predictive results need to be further validated through substantial experiments.

In conclusion, a radiotherapy-related four-gene methylation signature was identified for predicting HNSCC survival.

This platform may serve as a guide for the development of individualized therapy for patients with HNSCC. Translation of our findings into future clinical trials requires validation using large populations of patients.

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Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Authors' contributions

JM performed data analyses and wrote the manuscript. RL contributed significantly to data analyses and manuscript revision. JW conceived and designed the study. All authors read and approved the manuscript, and agree to be accountable for all aspects of the research in ensuring that the accuracy or integrity of any part of the work are appropriately investigated and resolved.

Ethics approval and consent to participate

In the original article of the datasets, the trials were approved by the local institutional review boards of all participating centers, and informed consent was obtained from all patients.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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